the base sequences being incapable of ligation to each other, wherein the contacting is carried out in the presence of ligase under conditions to ligate to the double-stranded portion of each DNA the probe bearing the base sequence complementary to the single-stranded DNA adjacent the double-stranded portion thereby to form an extended doublestranded portion which is incapable of ligation to further probes; and

(c) removing all unligated probes; followed by the steps of:

(d) cleaving the ligated probes to release each label;

(e) recording the quantity of each label; and

(f) activating the extended double-stranded portion to enable ligation thereto; wherein

(g) steps (b) to (f) are repeated in a cycle for a sufficient number of times to determine the sequence of each single-stranded DNA by determining the sequence of release of each label.

22. A method according to claim 21, wherein the array comprises a plurality of sub-arrays which together contain all the possible base sequences, and wherein each sub-array is contacted with the DNA population according to step (b), unligated probes are removed according to step (c), and these steps are repeated in a cycle before step (d) so that all of the subarrays contact the DNA population.

23. A method according to claim 21, wherein the target DNA population is obtained by sorting an initial DNA sample into sub-populations and selecting one of the subpopulations as the target DNA population.

24. A method according to claim 23, wherein the initial DNA sample is cut into fragments, each having a sticky end of known length and unknown sequence, which fragments are sorted into sub-populations according to their sticky end sequence.

25. A method according to claim 21, wherein each single-stranded DNA is immobilized at one end.

26. A method according to claim 21, wherein the label of each probe comprises a mass label, and the quantity of each label is recorded according to step (e) using mass spectrometry after release of the label in step (d).

27. A method according to claim 21, wherein the known base sequence is blocked at its 3'OH.

28. A method according to claim 27, wherein the step (d) of cleaving the ligated probes to release each label unblocks the 3'-OH of the extended double-stranded portion according to step (f).

29. A method according to claim 28, wherein the label of each probe is cleavably attached to the 3'-OH of the base sequence.

30. A method according to claim 21, wherein the base sequence of each probe is unphosphorylated at both 3' and 5' ends and step (f) comprises phosphorylating the 5'-OH of the extended double-stranded portion.

31. A method according to claim 21, wherein the predetermined length of the base sequence is from 2 to 6.

32. A method according to claim 31, wherein the predetermined length of the base sequence is 4.

33. A kit for sequencing DNA, which comprises an array of hybridization probes, each probe comprising a label cleavably attached to a known base sequence of predetermined length, the array containing all possible base sequences of that predetermined length and the base sequences being incapable of ligating to each other.

34. A kit according to claim 33, wherein the known base sequence is blocked at its 3'-OH.

35. A kit according to claim 34, wherein the label of each probe is cleavably attached to the 3'-OH of the base sequence to prevent ligation thereto.

36. A kit according to claim 33, wherein the base sequence of each probe is unphosphorylated at both 31 and 51 ends.

37. A kit according to claim 33, wherein the label of each probe comprises a mass label.

38. A kit according to claim 33, wherein the predetermined length of the base sequence is from 2 to 6.

39. A kit according to claim 38, wherein the predetermined length of the base sequence is 4.

~~40. Use of a kit as defined in claim 33 for a method of sequencing DNA.~~

REMARKS

The present Amendment is intended to eliminate the use of multiple dependency and to add an Abstract to the Specification.